



Biological Bases and Characterization in Oncogenes

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Abstract

Cancer is triggered by various things such as job, toxic chemicals, bacteria, the course of life, epithet geneticism and genetics. In genetics, oncogene, tumor suppressor and miRNA cause cancer. These genes are required to proliferate and separate regular cells, which lead to the abnormal expression in the cells. Modifications in the gene level involve mutation, translocation, rearrangement of DNA in the genes contributing to tumor activation and growth. The oncogenes and tumor suppressor genes are respective paradigms of Ras and p53. Oncogenes' properties include growth factors, receptors of growth factors, signal transducers, and nuclear transcription factors, which are the most popular anti-cancer drugs used to treat oncogene antibodies. MicroRNA has already proven its potential to be utilized in patient prognosis and in detection, which are the following cancer drug research priorities.

Key words: Tumours - Oncogenes - Mutants in Tumor Suppressor - miRNA - Cancer treatment

Introduction

Cancer and its causes: 12% of all deaths globally are currently triggered by cancer. Almost 12,000,000 cancers occurred in 2008 and about 6,000,000 cancer deaths worldwide[1]. This makes it the world's most significant cause of death and the second leading cause of death in the developed world. The prevalence of cancer is estimated at around 2,5 million in India, with more than 8, 00,000 new cases and 5,50,000 deaths annually worldwide due to this disease[2]. The major cancer places in India include oral,

kidney, esophagus, and stomach among men and the cervix, as well as breast and oral cavities among women.

A combination of environmental and hereditary factors induces disease. Cancer In the one hand, disease, heredity and spontaneous mutations are influenced by environment, lifestyle and diet. There is a finely balanced balance between growth-promoting and growth-restraining signals in normal cell growth, which only occurs when proliferation is required[3].

Tumor Types: Tumors are either benign or malignant to be categorized into two primary groups. Benign tumors seldom endanger life, grow inside a well-defined capsule that limits their size, retains the cell's properties and is hence generally clearly distinguished. Malignant tumors invade and spread surrounding tissues in the body to create further growths or metastases. This is always the life-threatening phase[4].

Armitage and Doll[5] concluded that carcinogenes are in six to 7-stage stages. The multi-stage evolutionary production of carcinogen. Tumors tend to be more aggressive in developing and, at 195°, foulds[6] observed that the creation of the tumor took place step by step by step, with each step of triggering, mutating or losing particular genes.

cancers come from a single cell with a history of growth advantages[6]. It is believed that some sort of genotoxic agent such as radiation or a chemical carcinogen often causes this initiation step. The cells here are phenotypically normal, but altered at the DNA stage.

Additional transformations that influence genes that control the creation of cells help to generate additional clones that are compatible with tumor cell growth. Finally, the creation of clones with metastatic potential is rendered feasible by more developments. Both of these occurrences would possibly make the cell

Classification of Cancer:

As has been appreciated over the years, cancer is not a particular illness, but a whole set of diseases that comprise at least 300 separate histological forms. On the basis of embryological sources of the original tumor cells, cancer cells are defined as follows.

- ❖ Carcinomas are epithelial in nature (ectodermal and endodermal) (ectodermal and endodermal).
- ❖ Sarcomas are formed from connective tissue (mesodermal) (mesodermal).
- ❖ Leukemias are from blood-forming cells.
- ❖ Melanomas originate from pigment cells (melanocytes) (melanocytes).
- ❖ Teratomas originate from germ cells or gonadal tissue.

Centered on the genetic mutation cancer can also be divided into four primary classes:

- ❖ Many cancers are intermittent and environmental factors, such as toxins and radiation, caused. These cancers mutations are only found in the cancer tissue itself.
- ❖ These tumors have evident disease clustering
- ❖ family attributes rather than genetic illness to the shared setting for family members.

More chaotic, such that subsequent changes are likely to increase. Animal models of carcinogenesis, based primarily on patterns of skin cancer development in mice, have

allowed this to be divided into initiation, advancement, malignancy and metastatic disease [7]. Although it is evident that multiple improvements are needed to produce the tumor, it is not clear if the order in which the changes are necessary.

The multiple stages of cancer in the development of metagenes: the formation of cancer. Until A small proportion of cancers had a genetic cause well identified. The genes concerned have, in addition, a wider significance since the genes that activate this disorder are often the same as the genes that are active in the disease's sporadic phase. This is usually done in the DC gene, which is also the first gene to be mutated in development of sporadic colorectal cancer, since it was responsible for the hereditary disorder family adenomatous polyposis (FAP). The only exception to this rule is the inherited breast cancer induced in the BRCA1 and BRCA2 genes by mutations. Intermittent breast cancer has not detected defects in these genes to date. Causative defects arise in all cells of the body in tumors with a genuine hereditary basis. In this group, different tumors in patients and the condition should be identified at an early point in the life of individuals in a Mendelian manner[8].

- ❖ People with particular conditions, also referred to as chromosomal abnormalities, are at greater risk of cancer owing to the high fragility of chromosome present in cultured cells such as the xeroderma pigmentosum and ataxia telang ictas ia, although cancer happens fewer like patients in group 3.

Environmental and Epigenetic Factors:

It is apparent that cancer is not only a spontaneous alteration of the hereditary structure and wilderness of cells. Important factors such as smoking (lung cancer), multiple environmental mutages of potential cancer (agents which can boost the likelihood of cancer), dietary fat (cooling cancer) are non-genomic variables, etc (colon cancer). In addition to environmental elements, it is suspected that such epigenetic variables impact cancer rates[9].

For example, numerous types of carcinoma express the alpha-fetal protein (AFP) gene (AFP). This gene normally exists before and after the initiation of embryogenes. This represents a condition in which a gene is activated in the wrong place and at the wrong time. It is shown to be fully normal when the AFP gene is checked.

There are aberrant signals sent to the gene. In certain cases, retinal degeneration is documented in patients with small lung cell carcinomas. It is clarified that the carcinoma cells appear to display a natural differentiating antigen in the retinal cells on their surfaces during development. The antigen in such cells is seen by the immune system at the wrong spot and at the wrong time. A majority of the tumor cells are destroyed by anticorps, but the retina remains killed. Many of the pathophysiological effects of cancer are also the result of inaccurate tumor messages[10].

Cancer gene:

variations in oncogenes, genes of tumor suppressor and microRNA genes have contributed to cancer. Around 100 of our 50,000-100,000 genes have been identified in proto-oncogenes and around one dozen as tumor suppressor genes[11].

It is also possible to establish new targets for cancer by recognizing that most known oncogenes and tumor suppressors are components of a couple of common signal pathways controlling cell cycles, apoptosis, genome integrity, morphogenetic responses and cell differentiation.

Tumor Suppressor Genes:

Cellular genes are the second group of genes that perform an essential part in tumor genes (antioncogene, recessive tumor genes). These genes are involved in regulating abnormal cell proliferation and cancer is a leading fault or inactivation. They function, therefore, inhibiting or braking cell growth and cell cycling effectively. These genes are recessive at the process of cells but, together with a familiar cancer phenotype, have a dominant ancestry. Before the tumors grow, both gene variants must be mutated.

Classifying genes for tumor suppressors is more complex than oncogenes. There are now several dozen tumor suppressors linked to human cancers; TP53 (Brain, Breast, Colorectal and several cancer types), APC (adenomatous polyposis coli), BRCA1 and 2 (familial breast-ovarian carcinoma), RBI (Retinoblastoma), WT1 (Wilms' tumor), NF1 (Neurofibromatosis), TSC1, and 5C2 (Tubero's sclerosis), PTCH (Gorlin's syndrome or basal ce) have also been identified.

MicroRNAs (miRNAs): MicroRNAs, also known as gene expression micromanagers are evolutionarily retained miniscule noncoding RNAs. Unlike other genes involved in cancer [12].

codes proteins

codes proteins. These genes contain a single RNA strand of roughly 21 to 23 nucleotides. MicroRNA molecule may be annealed by blocking protein transmission and transcription and regulating gene expression to messenger RNA (mRNA) with a nucleotide sequence that complements the microRNA sequence. Examples of miR-15a and miR-16-1 are lymphocytic leukemias that show an early outbreak of this disease pathogenesis [13].

The areas of the genome that are also involved in the reorganization of chromosomes in cancer cells without oncogenes or genes that kill tumors appear to include genes with microrNA. Polymorphisms and expressive profiling [1° -19] are essential tools for studying disease's genetics since they have signature genes for multiple cancers in the miRNA pathway (miR-polymorphisms). Also with the intensive usage of miRNA microarrays, a number of miRNAs has been established as potential cancer biomarkers. Many miRNAs are classified for acting as oncogenes, tumor suppressors or cancer stem cell modulators and metastasis. Therefore miRNA is now an alternative in the prediction and diagnosis of cancer[13].

Oncogene:

Oncogene is a protein coding eukaryotic gene that has been preserved in existence and is likely to play a major physiological function in normal cells that have a potential to be an oncogenic determinant in the future [14]. The virus Avian sarcoma, called src, was first

discovered to be Oncogenes, and the oncogenes were called v-oncogenes (v-one) (v-one). J. The 1989 Nobel prize in medicine for discovering cellular origins of viral oncogenic oncogenes was awarded to Michael Bishop and Harold Varmus of the UCSF. Standard nononcogenic alleles from genes such as protooncogenes are often referred to and mutant alleles are referred to as active oncogenes[15].

The word active oncogene applies to the initiation of oncogenic behavior since the protooncogenes are expressed inside regular cells and therefore are active genes. Oncogenes are the genes of the cell or the virus (i.e. viral injections into the cell), and may contribute to neoplasm development.

Viruses and cancer: Viruses are infectious agents which need to increase in the host cell. Table 2 offers descriptions of some of the viruses that sustain human cancer.

Oncogene system of identification: mechanisms used include amplification (eg. ERBB2, MYCL, MYCN), chromosome translocation (ABL, BCL1, BCL2, MYC), retroviral homology (HRAS, KRAS, SRC), transfection (MAS, MET, MyC, RAS) [16].

Activation of proto-oncogenes:

Oncogene properties: proto-oncogenes facilitate cell growth and differentiation. They are coding four kinds of oncoproteins that facilitate cell division.

Factors of production

The growth factors involve the growth factor (PDGF), the epidermal growth factor (EGF), the growth factor for fibroblasts (1-° FGF), growth factors like insulin (IGFIs and 2) and the growth factor transformer (NTG and §) [25]. Growth factors Development factors are also included. Creature Factor Receptors The second class of oncoproteins included an epidermal growth factor family ([EGFR] erbB-2, erbB-3 and erbB-4), classified as HER1fi, PDGF-R and angiotensin receptors, and Platelet mediated growth factor receptors, are also labeled as HER1fi. A HER2 (Herceptin) antibody for breast cancer has been extensively tested[17].

A monoclonal antibody against the receptor extracellular domain (cetuximab) has been created, as well as competitive receptor tyrosine kinase inhibitors (e.g. erlotinib and gefitinib) (e.g., erlotinib and gefitinib). Bevacizumab is a monoclonal VEGF antibody, and SU5412, a small molecule binding VEGFR1 and VEGFR2 tyrosine kinase receptor, along with PDGF receptor and Package physiotherapy. Apparently, imatinib also inhibits PDgf and KIT receptor kinases as well as inhibits ABL kinase. Gastrointestinal stromal tumors bearing Package mutations triggering respond to the receptor kinases' imatinib or other inhibitors.

Serine/threonine kinases instead of tyrosin kinases are converting growth factor receptors. The tyrosine kinases are made up of a receptor with a ligand-related, extracellular domain, a transmembrane domain and a catalytic kinase intracellular domains that transmit the mitogenic signal [18].

Signal Transducers: Certain oncogenes encode signal pathway members. The two largest classes came together: non-receptor protein kinases and guanosine triphosphate proteins [19]. Two groups are NPK: tyrosine (for example: ABL, LCK and SRC) and serin, and threonine kinases. NPK are kinases of two distinct types (e.g., AKT, RAF1, MOS and PIM1). (AKT, RAF1, MOS and PIM1, for example). Nucleotide-binding proteins include RAS, GAS, and GIP. ABL, SRC, FES, FGR, SYN, and LCK comprise membrane/cytoplasmic protein kinases. Serine-threonine kinases consist of RAF, MOS and COT cytoplasmic protein.

Many of the above-mentioned receptors are fitted with standard signaling paths by which they relay messages, whereas there are three major pathways for intracellular signal transduction [20]. The following routes are the PI3-Kinase (PI3-K)/AKT route, the RAS/MAPK route and the JAK/Signal Transducers/Transcription Activator (STAT) pathway. When they bear activating mutations, proteins involved in signal transduction are oncogenic.

Nuclear transcription factors: transcription factors are ultimately triggered by signals originating in cytoplasmic signaling molecules. Factors of transcription bind DNA and initiate downstream gene transcriptions. Oncogene transcription factor in human cancers is not generally found to be mutated. In Burkitt's lymphoma for instance, proto-oncogen c-myc is converted into a sequence of IgG in B cells transcription, which is a chicken microcytomatosis virus. Since IgG is highly expressed in B-cells, this translocation contributes to massive over-expression c-myc ion that leads to tumorigenes [21].

In multigen groups, also transcription factors also include identical structural domains. This complex enhances the manifestation by several genes that control cell division and dimerizes, for example, the Fos transcription protein with a Jun transcription factor to the API transcription factor. The other transcription proteins that operate in the nucleus are MYC, FOS, JUN, MYB, SKI, EV11 and REL. Its effects also enhance the expression of the target genes with DNA and transcriptions. Their effects on activation are also phosphorylation. In the end, the cause of these genes supplies the resources and fuel for the proliferation and separation of cancer cells. Table 4 indicates the oncogenes active in and manner of activation of human cancer [22].

Oncogenes as Targets: In the background of human tumorigenesis, genes involving known oncogenes have been identified because of their homology. Due to advancement in molecular biology, separate, untransformed cells expressed tumorigenes associated genes. In vitro, testing of cells which express the genes has been carried out to evaluate motility, invasion and anchorage-independent development. These methods became repetitive since only one gene could be analyzed concurrently.

Many genes have today been easily studied through the cloning method, the genes expressed by cancer cells have been cloned into viruses and their properties have been checked and the gene responsible extracted[23]. Microarrays are another multigene process.

This technique is used for the examination of a glass slide (a chip), containing fragments of as many as 64,000 genes, isolated from a normal cell and cancer cell. The intensity of the different colors or mixture hues indicates that a gene in cancer cells is above or below the word. Protein microarrays have recently been created, where anticorps are located on a glass slide and proteins are labeled from normal and tumor cells. Again, the intensity of color indicates which proteins are above or under in cancer cells expressed.

This method is beneficial since many genes may also be identified at once, since it is less time consuming. In certain subsets of tumors, the microarrays may also contain tumor signatures: genes that are released. This tumor signatures will be used in the future to classify cancers which could contribute to a certain medicine, providing individual counseling for the patient with cancer[24].

Cancer Therapeutics By Oncogenes: The latest screening methods for gene research including cancer have triggered a substantial increase in potential molecular targets of cancer. Because of improvement in the study of oncogenes, there was a 61% growth from just 8% in the years 1996-2001 from 19th and 1983, to 61% in phase I tests, which were accepted later by the Food and Drug Administration (FDA). Some of the more recent molecular medicines are antibodies that prohibit transformative proteins from triggering. In contrast, monoclonal antibodies are wide and cannot penetrate the tumor site or move through the exterior tumor layers[25].

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